

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MOORE, PAUL A.
RUBEN, STEVEN M.
EBNER, REINHARD
- (ii) TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
(B) STREET: 9410 KEY WEST AVENUE
(C) CITY: ROCKVILLE
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: BROOKES, ANDERS A.
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF378
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 124..913
- (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 124..184
- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 187..913

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTACCAGAAC AGCATAACAA GGGCAGGTCT GACTGCAAGC TGGGACTGGG AGGCAGAGCC 60
 GCCGCCAAGG GGGCCTCGGT TAAACACTGG TCGTTCAATC ACCTGCAAGA CGAAGAGGCA 120
 AGG ATG CTG TTG GCC TGG GTA CAA GCA TTC CTC GTC AGC AAC ATG CTC 168
 Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu
 -21 -20 -15 -10
 CTA GCA GAA GCC TAT GGA TCT GGA GGC TGT TTC TGG GAC AAC GGC CAC 216
 Leu Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His
 -5 1 5 10
 CTG TAC CGG GAG GAC CAG ACC TCC CCC GCG CCG GGC CTC CGC TGC CTC 264
 Leu Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu
 15 20 25
 AAC TGG CTG GAC GCG CAG AGC GGG CTG GCC TCG GCC CCC GTG TCG GGG 312
 Asn Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly
 30 35 40
 GCC GGC AAT CAC AGT TAC TGC CGA AAC CCG GAC GAG GAC CCG CGC GGG 360
 Ala Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Arg Gly
 45 50 55
 CCC TGG TGC TAC GTC AGT GGC GAG GCC GGC GTC CCT GAG AAA CGG CCT 408
 Pro Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro
 60 65 70
 TGC GAG GAC CTG CGC TGT CCA GAG ACC ACC TCC CAG GCC CTG CCA GCC 456
 Cys Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala
 75 80 85 90
 TTC ACG ACA GAA ATC CAG GAA GCG TCT GAA GGG CCA GGT GCA GAT GAG 504
 Phe Thr Thr Glu Ile Gln Glu Ala Ser Glu Gly Pro Gly Ala Asp Glu
 95 100 105
 GTG CAG GTG TTC GCT CCT GCC AAC GCC CTG CCC GCT CGG AGT GAG GCG 552
 Val Gln Val Phe Ala Pro Ala Asn Ala Leu Pro Ala Arg Ser Glu Ala
 110 115 120
 GCA GCT GTG CAG CCA GTG ATT GGG ATC AGG CAG CGG GTG CGG ATG AAC 600
 Ala Ala Val Gln Pro Val Ile Gly Ile Ser Gln Arg Val Arg Met Asn
 125 130 135
 TCC AAG GAG AAA AAG GAC CTG GGA ACT CTG GGC TAC GTG CTG GGC ATT 648
 Ser Lys Glu Lys Lys Asp Leu Gly Thr Leu Gly Tyr Val Leu Gly Ile
 140 145 150
 ACC ATG ATG GTG ATC ATC ATT GCC ATC GGA GCT GGC ATC ATC TTG GGC 696
 Thr Met Met Val Ile Ile Ile Ala Ile Gly Ala Gly Ile Ile Leu Gly
 155 160 165 170
 TAC TCC TAC AAG AGG GGG AAG GAT TTG AAA GAA CAG CAT GAT CAG AAA 744
 Tyr Ser Tyr Lys Arg Gly Lys Asp Leu Lys Glu Gln His Asp Gln Lys
 175 180 185
 GTA TGT GAG AGG GAG ATG CAG CGA ATC ACT CTG CCC TTG TCT GCC TTC 792
 Val Cys Glu Arg Glu Met Gln Arg Ile Thr Leu Pro Leu Ser Ala Phe
 190 195 200
 ACC AAC CCC ACC TGT GAG ATT GTG GAT GAG AAG ACT GTC GTG GTC CAC 840
 Thr Asn Pro Thr Cys Glu Ile Val Asp Glu Lys Thr Val Val Val His
 205 210 215

364350-7013500

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ACC AGC CAG ACT CCA GTT GAC CCT CAG GAG GGC AGC ACC CCC CTT ATG 888
 Thr Ser Gln Thr Pro Val Asp Pro Gln Glu Gly Ser Thr Pro Leu Met
 220 225 230

GGC CAG GCC GGG ACT CCT GGG GCC T GAGCCCCCCC AGTGGGCAGG 933
 Gly Gln Ala Gly Thr Pro Gly Ala
 235 240

AGCCCATGCA GACACTGGTG CAGGACAGCC CACCCTCCTA CAGCTAGGAG GAACTACCAC 993

TTTGTGTTCT GGTAAACC CTACCACTCC CCCGCTTTTT TGGCGAATCC TAGTAAGAGT 1053

GACAGAAGCA GGTGGCCCTG TGGGCTGAGG GTAAGGCTGG GTAGGGTCCT AACAGTGCTC 1113

CTTGTCATC CTTGGAGCA GATTTGTCT GTGGATGGAG ACAGTGGCAG CTCCACAGT 1173

GATGCTGCTG CTAAGGGCTT CCAAACATTG CCTGCACCCC TGGAACTGAA CCAGGGATAG 1233

ACGGGGAGCT CCCCAGGCT CCTCTGTGCT TTACTAAGAT GGCTCAGTCT CCACTGTGGG 1293

CTTGAGTGGC ATACACTGTT ATTCATGGTT AAGGTAAAGC AGGTCAAGGG ATGGCATTGA 1353

AAAAATATAT TTAGTTTTTA AAATATTTGG GATGGAAGTC CTTACTGACC TCTGACAACT 1413

GGAAACGAGT TTGTACTGAA GTCAGAACTT TGGGTTGGGA ATGAGATCTA GGTGTGGCT 1473

GCTGGTATGC TTCAGCTTGC TGGCAATGAT GTGCCTTGAC AACCGTGGGC CAGGCCTGGG 1533

CCCAGGGACT CTTCTGTTT CATAAGGAAA GGAAGAATTG CACTGAGCAT TCCACTTAGG 1593

AAGAGGATAG AGAAGGATCT GCTCCGCCTT TGGCCACAGG AGCAGAGGCA GACCTGGGAT 1653

GCCCCAGTTT CTCTTCAGGG ATGGATAGTG ACCTGTCTTC ATTTTGACA GGTAAGAGAG 1713

TAGTTAGCTA ACCTATGGGA ATTATACTGT GGGGCCTTGT GAGCTGCTTC TAAGAGGCTA 1773

ACCTGGAAAC TAAGCTCAGA GGCAAGGTAA TAAAGCACTT CAGGGCTTGC TCCCCAAGTG 1833

GGCTGATTT AGCAGGTGGT CTGCGGGCGT CCAGGTCAGC ACCTTCCTGT AGGGCACTGG 1893

GGCTAGGGTC ACAGCCCCTA ACTCATAAAG CAATCAAAGA ACCATTAGAA AGGGCTCATT 1953

AAGCCTTTTG GACACAGGAC CCCAGAGAGG AAAAAGTGAC TTGCCCAAGG TCGTAAGCAA 2013

GCTACTGGCA TGGCAAGAGC CCAGCTTCCT GACGGAGCGC AACATTTCTC CACTGCACTG 2073

TGCTAGCAGC TCAGCAGGGC CTCTAACCTG TGATGTCACA CTCAAGAGGC CTTGGCAGCT 2133

CCTAGCCATA GAGCTTCCTT TCCAGAACCC TTCCACTGCC CAATGTGGAG ACAGGGGTTA 2193

GTGGGGCTTT CTATGGAGCC ATCTGCTTTG GGGACCTAGA CCTCAGGTGG TCTCTGGTG 2253

TTAGTGATGC TGGAGAAGAG AATATTACTG GTTCTACTT TTCTATAAAG GCATTCTCT 2313

ATAAAAAAAAA AAAAAA 2329

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

662350-16143060

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
 -21 -20 -15 -10

Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
 -5 1 5 10

Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
 15 20 25

Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly Ala
 30 35 40

Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Arg Gly Pro
 45 50 55

Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro Cys
 60 65 70 75

Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala Phe
 80 85 90

Thr Thr Glu Ile Gln Glu Ala Ser Glu Gly Pro Gly Ala Asp Glu Val
 95 100 105

Gln Val Phe Ala Pro Ala Asn Ala Leu Pro Ala Arg Ser Glu Ala Ala
 110 115 120

Ala Val Gln Pro Val Ile Gly Ile Ser Gln Arg Val Arg Met Asn Ser
 125 130 135

Lys Glu Lys Lys Asp Leu Gly Thr Leu Gly Tyr Val Leu Gly Ile Thr
 140 145 150 155

Met Met Val Ile Ile Ile Ala Ile Gly Ala Gly Ile Ile Leu Gly Tyr
 160 165 170

Ser Tyr Lys Arg Gly Lys Asp Leu Lys Glu Gln His Asp Gln Lys Val
 175 180 185

Cys Glu Arg Glu Met Gln Arg Ile Thr Leu Pro Leu Ser Ala Phe Thr
 190 195 200

Asn Pro Thr Cys Glu Ile Val Asp Glu Lys Thr Val Val Val His Thr
 205 210 215

Ser Gln Thr Pro Val Asp Pro Gln Glu Gly Ser Thr Pro Leu Met Gly
 220 225 230 235

Gln Ala Gly Thr Pro Gly Ala
 240

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

362330-164860

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro
 1 5 10 15
 Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala
 20 25 30
 Tyr Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro
 35 40 45
 Trp Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro
 50 55 60
 Ser Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro
 65 70 75 80
 Asp Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu
 85 90 95
 Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg
 100 105 110
 Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp
 115 120 125
 Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg
 130 135 140
 Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys
 145 150 155 160
 Trp Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His
 165 170 175
 His Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu
 180 185 190
 Glu Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe
 195 200 205
 Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser
 210 215 220
 Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys
 225 230 235 240
 Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu
 245 250 255
 Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg
 260 265 270
 Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser
 275 280 285
 Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly
 290 295 300
 Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln
 305 310 315 320
 Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr
 325 330 335
 Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val

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340 345 350
 Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp
 355 360 365
 Asn Met Arg Pro
 370

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATTGCACTGA GCATTCCACT TAGGAAGAGG ATAGAGAAGG ATCTGCTCCG CCTTTGGCCA 60
 CAGGAGCAGA GGCAGACCTG GGATGCCCCA TTTCTCTTCA GGGATGGATA GTGACCTGTC 120
 TTCATTTTGC ACAGGTAAGA GAGTAGTTAG CTAACCTATG GGAATTATAC TGTGGGGCCT 180
 TGTAGCTGCT TCTAAGAGGC TAACCTGGAA ACTAAGCTCA GAGGCAAGGT AATAAAGCAC 240
 TTCAGGGCTT 250

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATAGAGAAAT GCCTTTATAG AAAAGTAGAA ACCAGTAATA TTCTCTTCTC CAGCATCACT 60
 AACACCAAGA GACCACCTGA GGTCTAGGTC CCCAAAGCAG ATGGCTCCAT AGAAAGCCCC 120
 ACTAACCCGT CTCCACATTG GGCAGTGGAA GGGTTCTGGA AAGGAAGCTC TATGGCTAGG 180
 AGCTGCCAAG GCCTCTTGAG TGTGACATCA CAGGTTAGAG GCCCTGCTGA GCTGCTAGCA 240
 CAGTGCA 247

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTCGGCAA GAGTAACAGC ATAACAAGGG TAGGTCTGAC TGCAGCTGGG ACTGGGAGGC 60
 AGAGCACGCC AAGGGGGCCT CGGTAAACA CTGGTCGTTT AATCACCTGC AAACGAGGAG 120
 GCAAGGATGC TGTGGGCTG GGTACAGCAT TCCTGGTCAG CAACATGCTC CTAGCGTAAG 180
 CCTATGGATC TGGAGGCTGT TTCTGGGACA ACGGCCACTG TACCCGGAGG ACCAGACCTT 240
 CCCGGCCGGT CCTCGTGCCT GAACTGGCTG GACGCGCAGG GCTGCCTGGG CCCCTTTTTC 300
 GGTCAAATTT CACAGTTTAC TTCGAAACCG GGACGGGGCC GTGGGGGCCC TGGTGGTTAG 360
 TTTGGGGTCG GGTTCCTTA AAAAGGTTT TTGGGGCCGG TTTTCGGAAC CATTCGGTT 420
 GAATTTTTTA GGGAAATTC AGGAGTTTTT TAAGGGCCAT T 461

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCAAGTTGC AGAACTGGAA ACGAGTTTGT ACAGAAGTCA GAACTTTGGG TTAGGAATGA 60
 GATCTAGGTT GTGGCTGCTG GTATGCTTCA TTGCTGGCAA TAATGTGCCT TGACAACCGT 120
 GGGCCAGGCC TGGGACCAGG GACTCTTCCT GTTTCATAAG GAAAGGAAGA ATTGCACTGA 180
 GCATTCCACT TAGGAAGAGG ATAGAGCAAG GAATCTGCTC CGCTTTGGCC ACAGGAGCAG 240
 AGGCAGACCT GGGATGCCCC AGTTCTCTTT CAGGGATGGG ATAGTGACCT GTCTTACATT 300
 TTGCACAGGT AAAGAGAGTT AGTTAGCTAA CCTATTGGGC TTTATTACTT GGGGCTTGTG 360
 AGCTGCTTTT TAAGAGGTTA ACCTGGAAC AAAGTTCAG 399

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

664250-1648000

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TAATTCGGCA AGGGACAGGT CTGACTGCAG CTGGGACTGG GAGGCAGAGC CGTCAAGGGG 60
 GCCTCGGTA AACACTGGTC GTTCAATCAC CTGCAACGAG AGGCAAGGAT GCTGTTGGCC 120
 TGGGTACAAG CATTCTGTG AGCAACATGC TCCTAGCAGA AAGCCTATGG ATCTGGGAGG 180
 CTGTTTCTGG GACAACGGCC ACCTGTACCG GAGGACCAGA CCTCCCCGGC CGGGCCTTCC 240
 GTGGCCTTCA ATTGGTTTGA CGTGGCAAAG GGGCTTGTCT GGCCCTTTTG GGGGAAAATT 300
 ACAAGTTTTA ATTGTCCCGG AAAACCTGGA GAGG 334

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTCGGCAG AGGGAGAGGG AGATGCAGCG AATCACTCTG CCCTTGTCTG CCTTCACCAA 60
 CCCCACCTGT GAGATTGTGG ATGAGAAGAC TGTCGTGGTC CACACCAGCC AGACTCCAGT 120
 TGACCCTCAG GAGGGCAGCA CCCCCCTTAT GGGACCAGGC CGGGGACTCC TGGGGCCTGA 180
 GCCCCCAGT GGGGCAGGAG CCATGGCAGA CACTGGTGCA GGACAGCCAC CCTCCTTACA 240
 GCTAGGGGGA ACTACCACTT TGTGTTTCTG GTTTAAAACC CTACCACTCC CGGATTTTTT 300
 GGCGGATTCC TTAGTTAAGA GTACAGAAGC AGGTGGGCCT ATGGCTTGGA GGGTAAGGTG 360
 GGGTAGGGTT CCTAAAAGTG GGTTCCTGGT TGCTCCTGGG AGGAAGATTT TGGTTTTGGT 420
 GGGGACAGTG GCAGTTTCCA CAGTTTGTG TGTAAAGGGG TTCAAAAAAT TG 472

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCACGAGA TGAACCTCAA GGAGAAAAAG GACCTGGGAA CTCTGGGTAT GACGGTCCCC 60
 CACCCCTGCC CTTGTTGGGA TTCATCAAGA GATGTCATTT GCTGATTGTC TAGGGTGTGG 120
 CTAATGGGAC CTTGTGTCCT ATCCTTGGCA GGCTACGTGC TGGGCATTAC CATGATGGTG 180
 ATCATCATTG CCATCGGAGC TGGCATCATC TTGGGCTACT CTACAAGAGG TCAGTAGCTT 240

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CTCTTCTGGG CCTCTTAGG AGGAGGGGAG GAAGGTACAC AAAGTCAAAC T

291

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGACATG TCTGGAGGCT GTTCTCTGG

28

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCGGAAGCT TATTAGGCC CAGGAGTCCC GGC

33

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCCGGGATC CGCCATCATG CTGTTGGCCT GGGTAC

36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCGGGTAC CTTATTAGGC CCCAGGAGTC CCGGC

35

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCCGGGATC CGCCATCATG CTGTTGGCCT GGGTAC

36

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCCGGGTAC CTTATTAGGC CCCAGGAGTC CCGGC

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GGCCGGGTAC CTTATTAGGC CCCAGGAGTC CCGGC